

RAW SEQUENCE LISTING DATE: 10/12/2004 PATENT APPLICATION: US/09/993,292B TIME: 12:06:10

Input Set : A:\09-993,292 Sequence Listing.txt Output Set: N:\CRF4\10122004\I993292B.raw

3 <110> APPLICANT: University of Maryland, Baltimore GALEN, James E. 6 <120> TITLE OF INVENTION: USE OF CLYA HEMOLYSIN FOR EXCRETION OF PROTEINS 8 <130> FILE REFERENCE: A8461 10 <140> CURRENT APPLICATION NUMBER: 09/993,292B 11 <141> CURRENT FILING DATE: 2001-11-23 13 <150> PRIOR APPLICATION NUMBER: US 60/252,516 14 <151> PRIOR FILING DATE: 2000-11-22 16 <160> NUMBER OF SEQ ID NOS: 28 18 <170> SOFTWARE: PatentIn version 3.3 20 <210> SEQ ID NO: 1 21 <211> LENGTH: 6271 22 <212> TYPE: DNA 23 <213 > ORGANISM: Artificial Sequence 25 <220> FEATURE: 26 <223> OTHER INFORMATION: pSEC84 Expression Plasmid 28 <400> SEQUENCE: 1 29 gaattetgtg gtagcacaga ataatgaaaa gtgtgtaaaag aagggtaaaa aaaaccgaat 60 31 gcgaggcatc cggttgaaat aggggtaaac agacattcag aaatgaatga cggtaataaa 120 33 taaagttaat gatgatagcg ggagttattc tagttgcgag tgaaggtttt gttttgacat 180 35 teagtgetgt caaataetta agaataagtt attgatttta acettgaatt attattgett 240 37 gatgttaggt gettattteg ecatteegea ataatettaa aaagtteeet tgeatttaca 300 39 ttttgaaaca tctatagcga taaatgaaac atcttaaaag ttttagtatc atattcgtgt 360 41 tggattattc tgcatttttg gggagaatgg acttgccgac tgattaatga gggttaatca 420 43 gtatgcagtg gcataaaaaa gcaaataaag gcatataaca gatcgatctt aaacatccac 480 45 aggaggatgg gatccaaaat aaggaggaaa aaaaaatgac tagtattttt gcagaacaaa 540 47 ctgtagaggt agttaaaagc gcgatcgaaa ccgcagatgg ggcattagat ctttataaca 600 49 aatacctcga ccaggtcatc ccctggaaga cctttgatga aaccataaaa gagttaagcc 660 51 gttttaaaca ggagtactcg caggaagctt ctgttttagt tggtgatatt aaagttttgc 720 780 55 tegtgaegea attactetea gegtatattt taetatttga tgaatataat gagaaaaaag 840 57 catcagecca gaaagacatt eteattagga tattagatga tggtgteaag aaactgaatg 900 59 aagegeaaaa ateteteetg acaaqtteae aaagttteaa caacqettee qqaaaactqe 960 61 tggcattaga tagccagtta actaatgatt tttcggaaaa aagtagttat ttccagtcac 1020 63 aggtggatag aattegtaag gaagettatg ceggtgetge ageeggeata gtegeeggte 1080 65 cgtttggatt aattatttcc tattctattg ctgcgggcgt gattgaaggg aaattgattc 1140 67 cagaattgaa taacaggeta aaaacagtge aaaatttett taetagetta teagetacag 1200 69 tgaaacaagc gaataaagat atcgatgcgg caaaattgaa attagccact gaaatagcag 1260 71 caattgggga gataaaaacg gaaaccgaaa caaccagatt ctacgttgat tatgatgatt 1320 73 taatgctttc tttattaaaa ggagctgcaa agaaaatgat taacacctgt aatgaatacc 1380 75 aacaacgtca tggtaagaag acgcttttcg aggttcctga cgtcgctagc tgataaccta 1440 77 gggccagcaa aaggccagga accgtaaaaa ggccgcgttg ctggcgtttt tccataggct 1500

79 ccgccccct gacgagcatc acaaaaatcg acgctcaagt cagaggtggc gaaacccgac

1560

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181 getgeeteec ggagtttgte tegageaett ttgttaceeg ceaaacaaaa cecaaaaaca
                                                                       4620
183 acccataccc aacccaataa aacaccaaaa caagacaaat aatcattgat tgatggttga
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4740
187 aaaaaaacac cataaggagt tttataaatg ttggtattca ttgatgacgg ttcaacaaac
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189 atcaaactac agtggcagga aagcgacgga acaattaaac agcacattag cccgaacaqc
191 ttcaaacgcg agtgggcagt ctcttttggt gataaaaagg tctttaacta cacactgaac
                                                                       4920
193 ggcgaacagt attcatttga tccaatcagc ccggatgctg tagtcacaac caatatcgca
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195 tggcaataca gcgacgttaa tgtcgttgca gtgcatcacg ccttactgac cagtggtctg
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197 ceggtaageg aagtggatat tgtttgeaca etteetetga eagagtatta egacaqaaat
                                                                       5100
199 aaccaaccca atacggaaaa tattgagcgt aagaaagcaa acttccggaa aaaaattaca
                                                                       5160
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211 aataactatc tgaagcaacg aattaatgat gagaacaaaa tatcaatagt caccgaagca
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213 atgaatgaag cacttegtaa aettgageaa egtgtattaa ataegeteaa tgaattttet
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217 aaacacaca agattegtga tgaaegtttt tteaaaacca ataactetea atatgattta
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                                                                       5760
221 aactaaatcc agatgtaaat caaacagata aaattgtttg tgatacactg gacagtatcc
                                                                       5820
223 cgcaagggga acgaagccgc cttaaccggg ccgcactgac ggcaggtctg gccttataca
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225 gacaagatcc ccggacccct ttccttttat gtgagctgct gacgaaagaa accacatttt
                                                                       5940
227 cagatategt gaatatattg agategetat ttecaaaaga gatggeegat tttaattett
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229 caatagtcac tcaatcctct tcacaacaag agcaaaaaag tgatgaagag accaaaaaaa
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231 atgcgatgaa gctaataaat taattcaatt attattgagt tccctttatc cactatcagg
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233 ctggataaag ggaactcaat caagttattt tettaccagt cattacataa tegttattat
                                                                       6180
235 gaaataatcg tttgcactgt ctctgttatt caggcaattt caataaaggc acttgctcac
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237 gctctgtcat tttctgaaac tcttcatgct g
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241 <211> LENGTH: 305
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251 Ile Glu Thr Ala Asp Gly Ala Leu Asp Leu Tyr Asn Lys Tyr Leu Asp
                                   25
255 Gln Val Ile Pro Trp Lys Thr Phe Asp Glu Thr Ile Lys Glu Leu Ser
259 Arg Phe Lys Gln Glu Tyr Ser Gln Glu Ala Ser Val Leu Val Gly Asp
263 Ile Lys Val Leu Leu Met Asp Ser Gln Asp Lys Tyr Phe Glu Ala Thr
264 65
                                           75
267 Gln Thr Val Tyr Glu Trp Cys Gly Val Val Thr Gln Leu Leu Ser Ala
                   85
                                       90
271 Tyr Ile Leu Leu Phe Asp Glu Tyr Asn Glu Lys Lys Ala Ser Ala Gln
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                                   105
                                                       110
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275 276	Lys	Asp	Ile 115	Leu	Ile	Arg	Ile	Leu 120	Asp	Asp	Gly	Val	Lys 125	Lys	Leu	Asn	
279 280	Glu	Ala 130	Gln	Lys	Ser	Leu	Leu 135	Thr	Ser	Ser	Gln	Ser 140	Phe	Asn	Asn	Ala	
283	Ser	Glv	Lvs	Leu	Leu	Ala		Asp	Ser	Gln	Leu		Asn	Asp	Phe	Ser	
	145		_1			150				0	155			1101	1110	160	
	Glu	Lvs	Ser	Ser	Tvr		Gln	Ser	Gln	Val		Ara	Tle	Ara	Lvs		
288		_1 -			165			~~-		170	1101	5		9	175	014	
	Ala	Tvr	Ala	Glv		Ala	Ala	Glv	Tle		Ala	Glv	Pro	Phe		Len	
292		-		180				1	185			- 1		190		-	
295	Ile	Ile	Ser		Ser	Ile	Ala	Ala		Val	Ile	Glu	Glv		Leu	Ile	
296			195	-				200					205	-2			
299	Pro	Glu	Leu	Asn	Asn	Arq	Leu	Lvs	Thr	Val	Gln	Asn		Phe	Thr	Ser	
300		210					215	-				220					
303	Leu	Ser	Ala	Thr	Val	Lys		Ala	Asn	Lvs	asp		Asp	Ala	Ala	Lvs	
	225					230					235					240	
	Leu	Lys	Leu	Ala	Thr		Ile	Ala	Ala	İle		Glu	Ile	Lvs	Thr		
308		-			245					250	-	•	-	1	255		
311	Thr	Glu	Thr	Thr	Arq	Phe	Tyr	Val	Asp		Asp	Asp	Leu	Met		Ser	
312				260	_		-		265	-	_			270			
315	Leu	Leu	Lys	Gly	Ala	Ala	Lys	Lys	Met	Ile	Asn	Thr	Cys		Glu	Tyr	
316			275	_			_	280					285			•	
319	Gln	Gln	Arg	His	Gly	Lys	Lys	Thr	Leu	Phe	Glu	Val	Pro	Asp	Val	Ala	
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323	Ser																
	305																
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360	<220	> FE	:ATUR	Œ:													

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369	<210> SEQ ID NO: 6				
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	<220> FEATURE:				
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	<210> SEQ ID NO: 7	•			,
	<211> LENGTH: 60				
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	<400> SEQUENCE: 7	. I I IIICI			
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VERIFICATION SUMMARY

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